FIG. 1

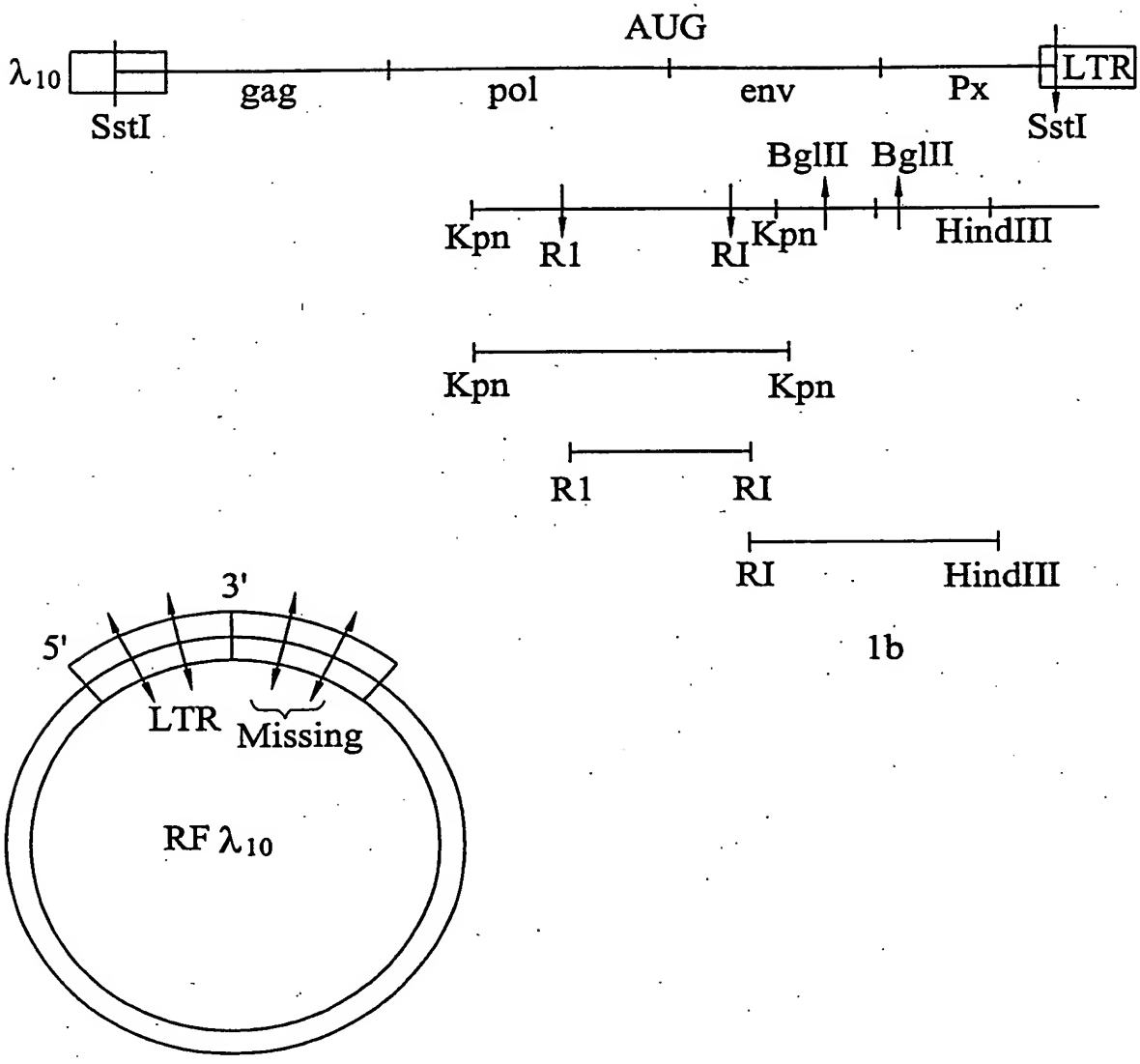

AUG
λ10
gag
pol
env
Px
LTR
SstI
SstI
BglII
BglII
Kpn
R1
RI
Kpn
HindIII
Kpn
Kpn
R1
RI
RI
HindIII
1b
3'
5'
LTR
Missing
RF λ10

FIG. 2

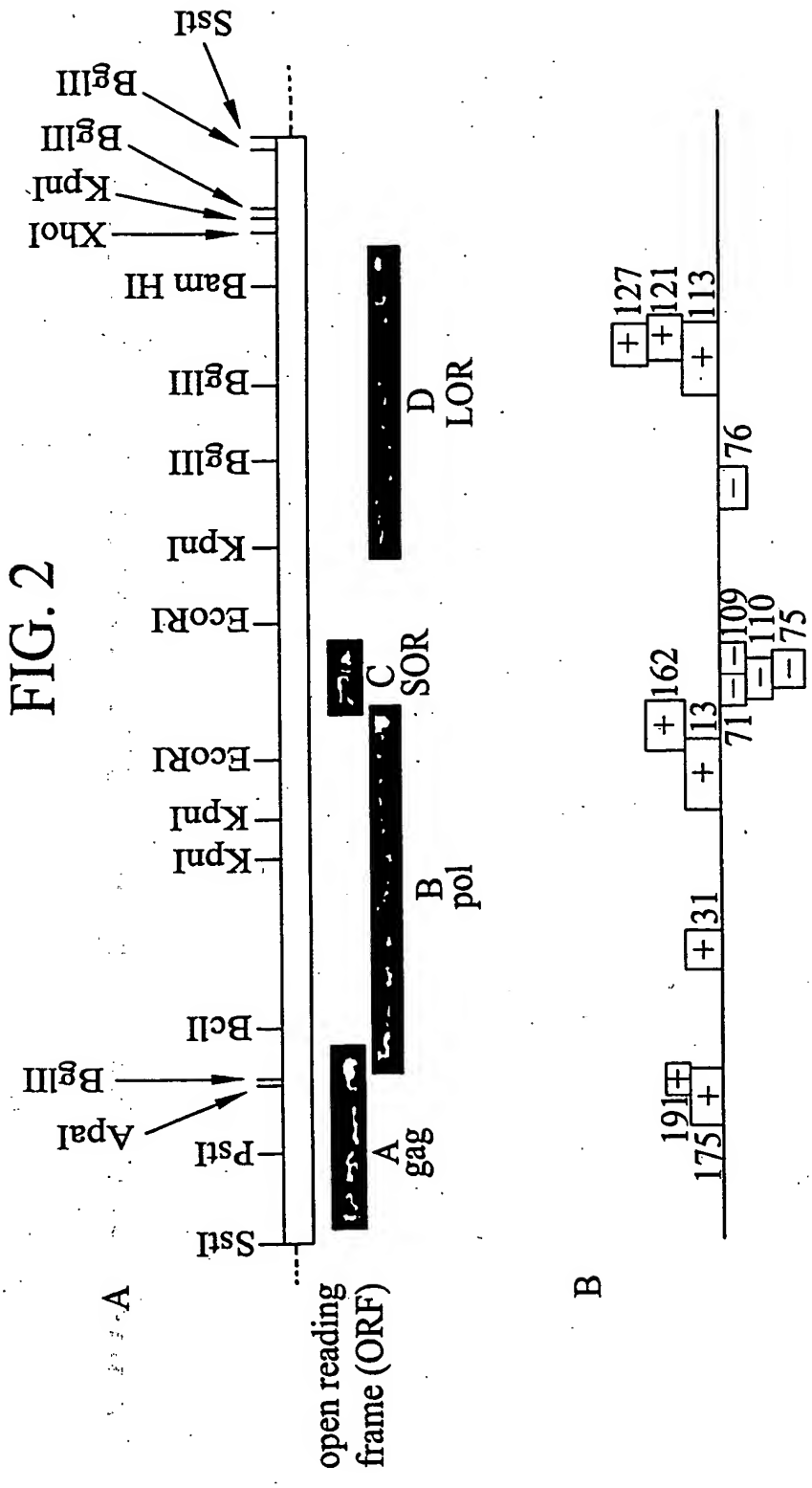

A
SstI
PstI
ApaI
BglII
BclI
KpnI
KpnI
KpnI
EcoRI
EcoRI
KpnI
BglII
BglII
Bam HI
XhoI
KpnI
BglII
BglII
A
gag
B
pol
C
SOR
D
LOR
open reading
frame (ORF)
B
175
191
+31
+13
+162
71
109
110
75
76
+113
+121
+127

FIG. 3

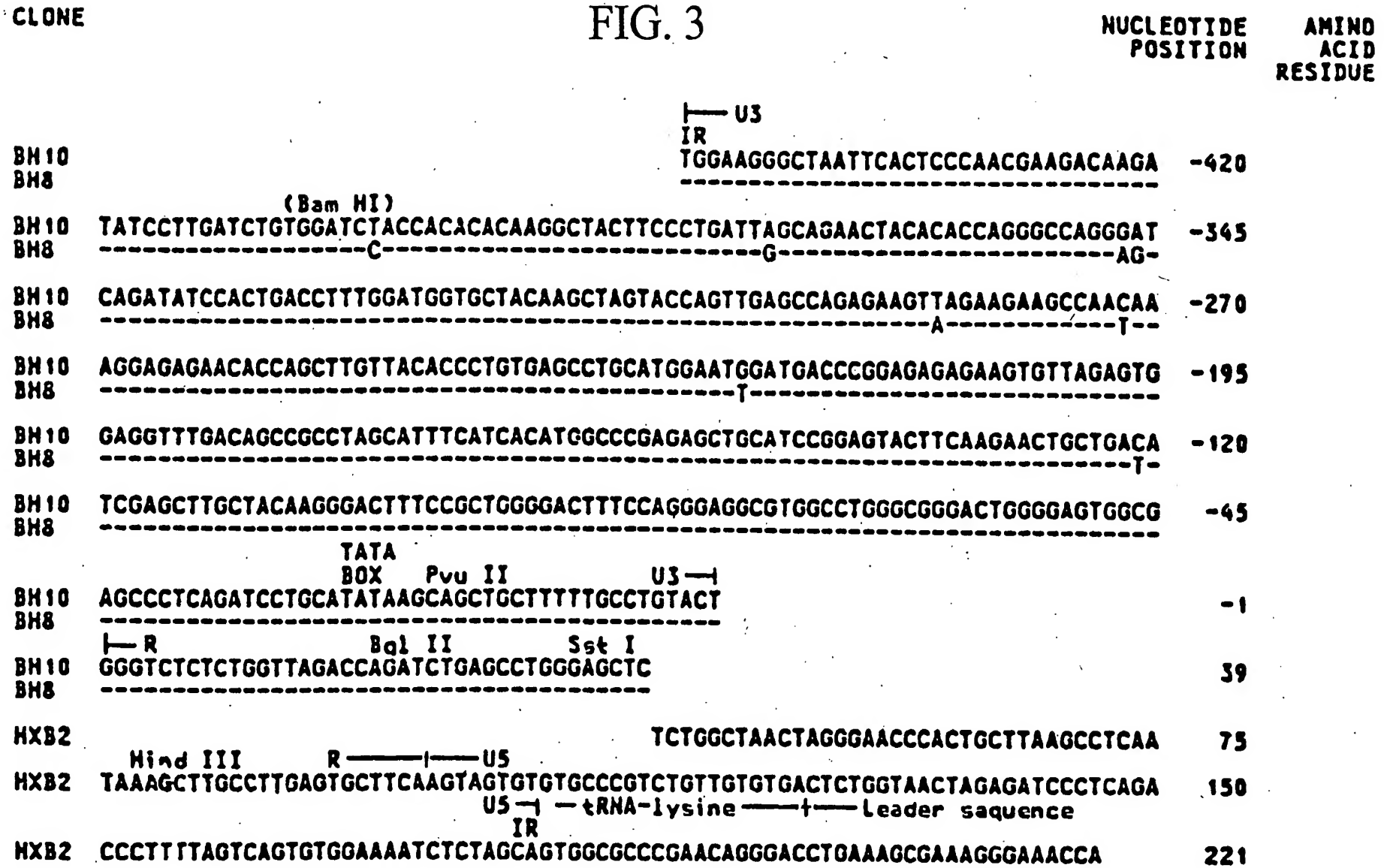


FIG. 3 (Continued)

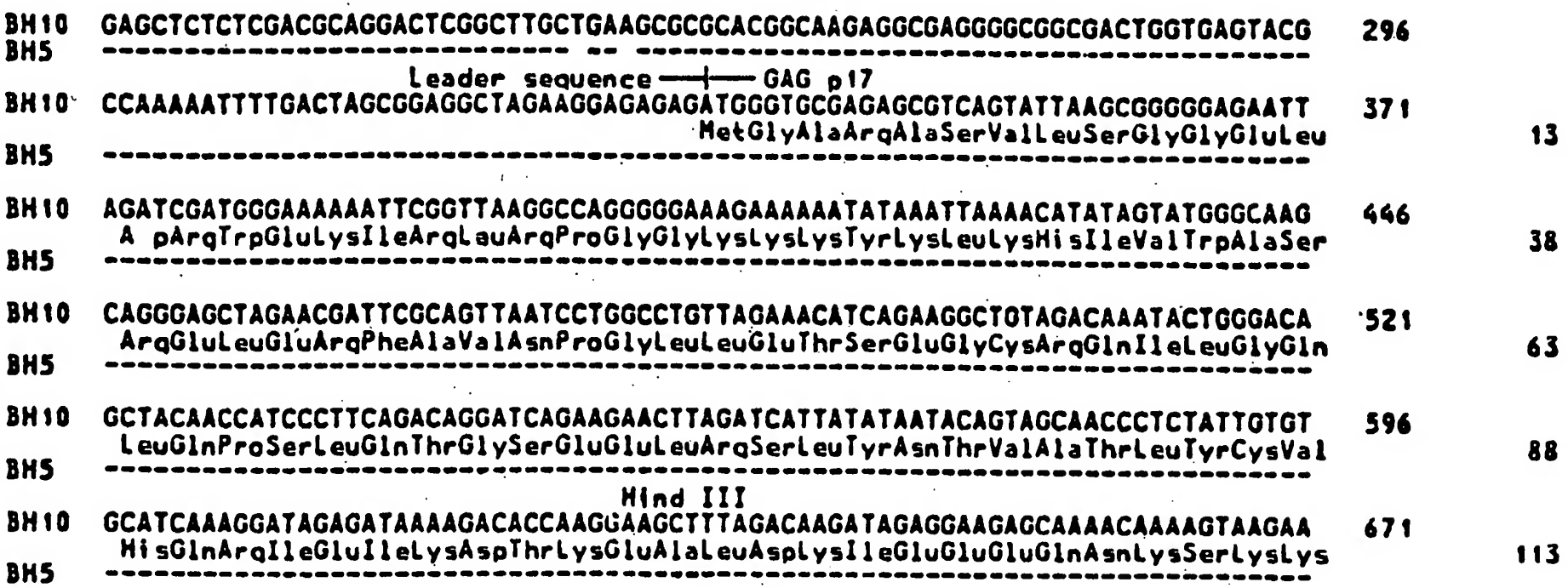


FIG. 3 (Continued)

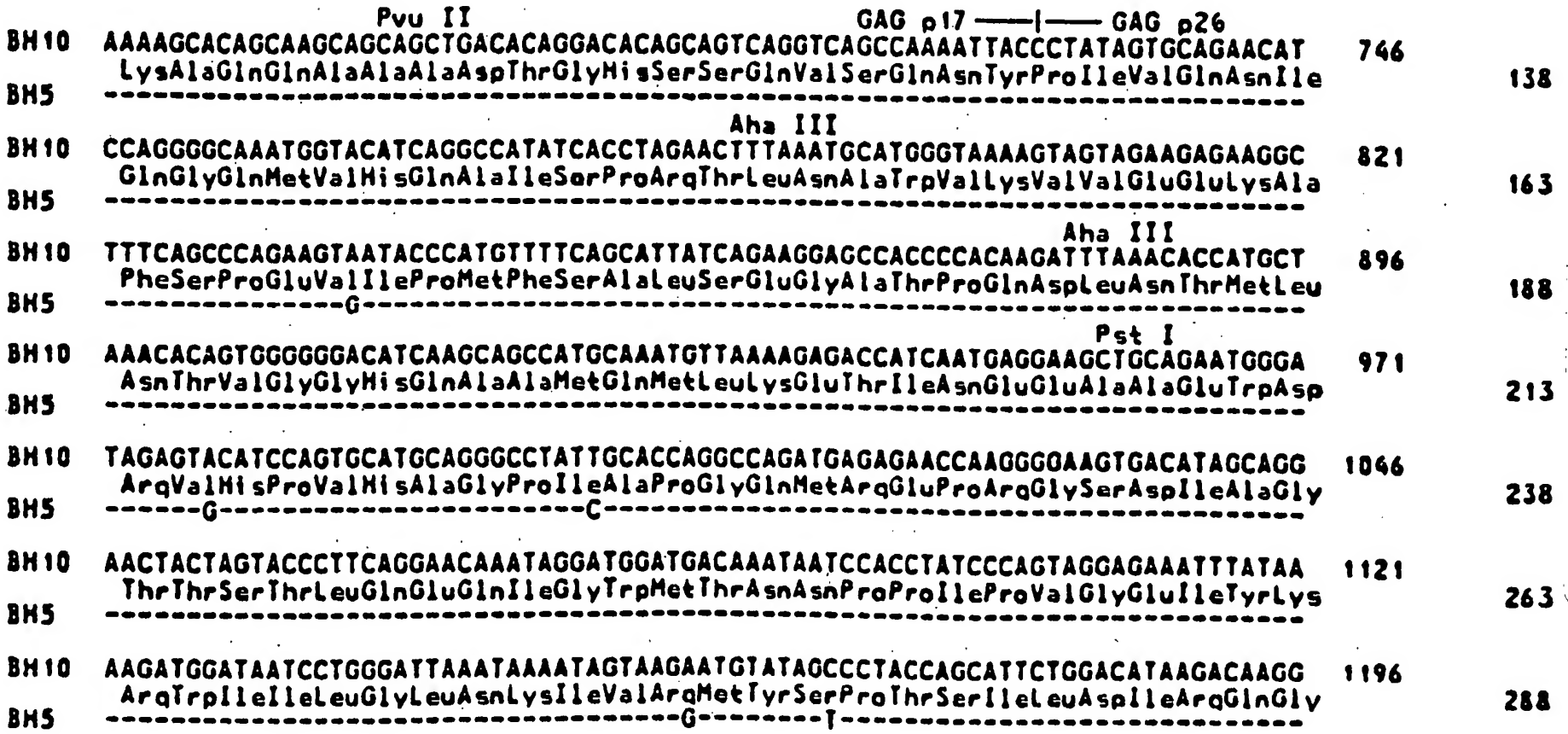
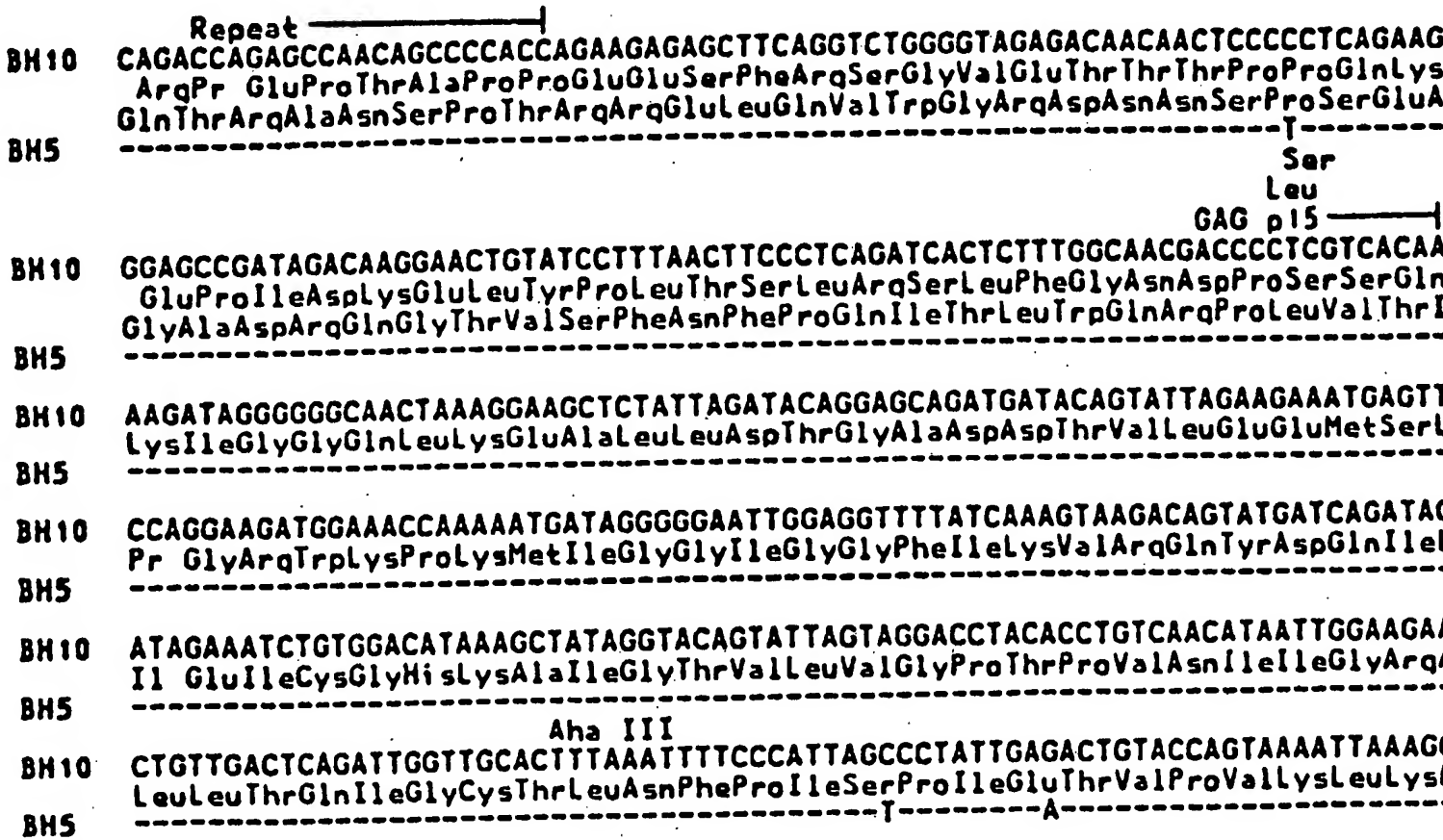


FIG. 3 (Continued)

FIG. 3 (Continued)



1796 488 56
1871 512 81
1946 106
2021 131
2096 156
2171 181

FIG. 3 (Continued)

FIG. 3 (Continued)

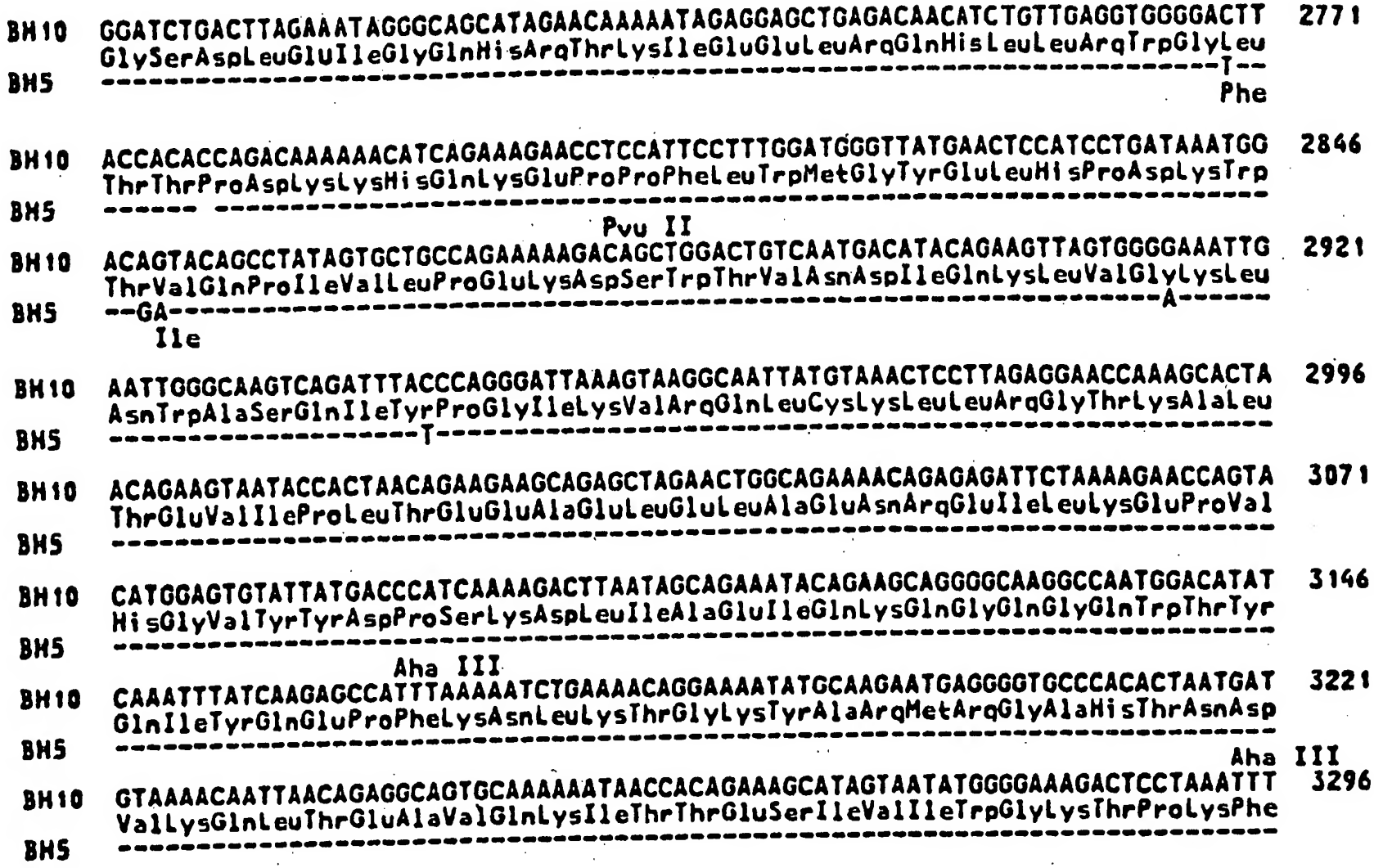


FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

FIG. 3 (Continued)

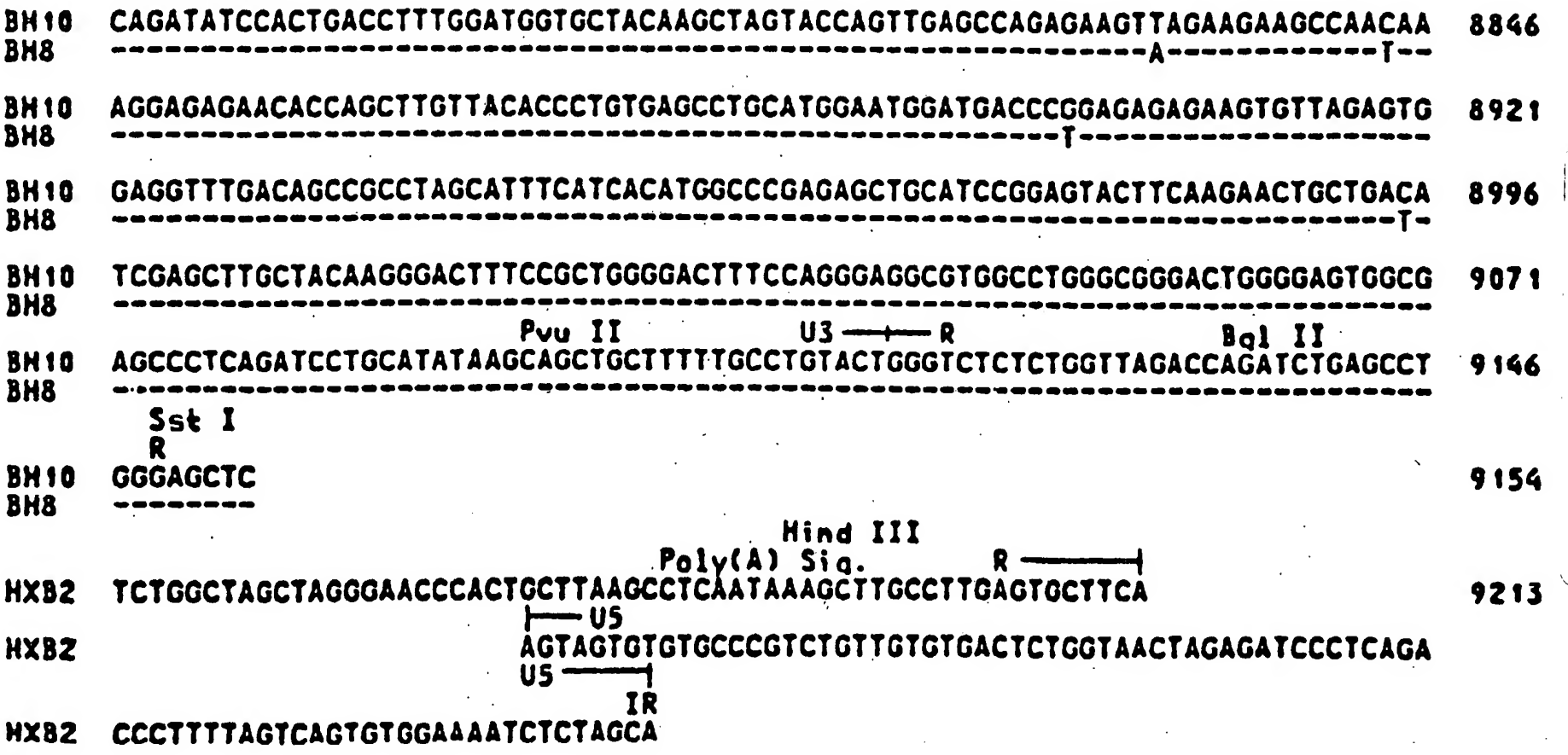


FIG. 4

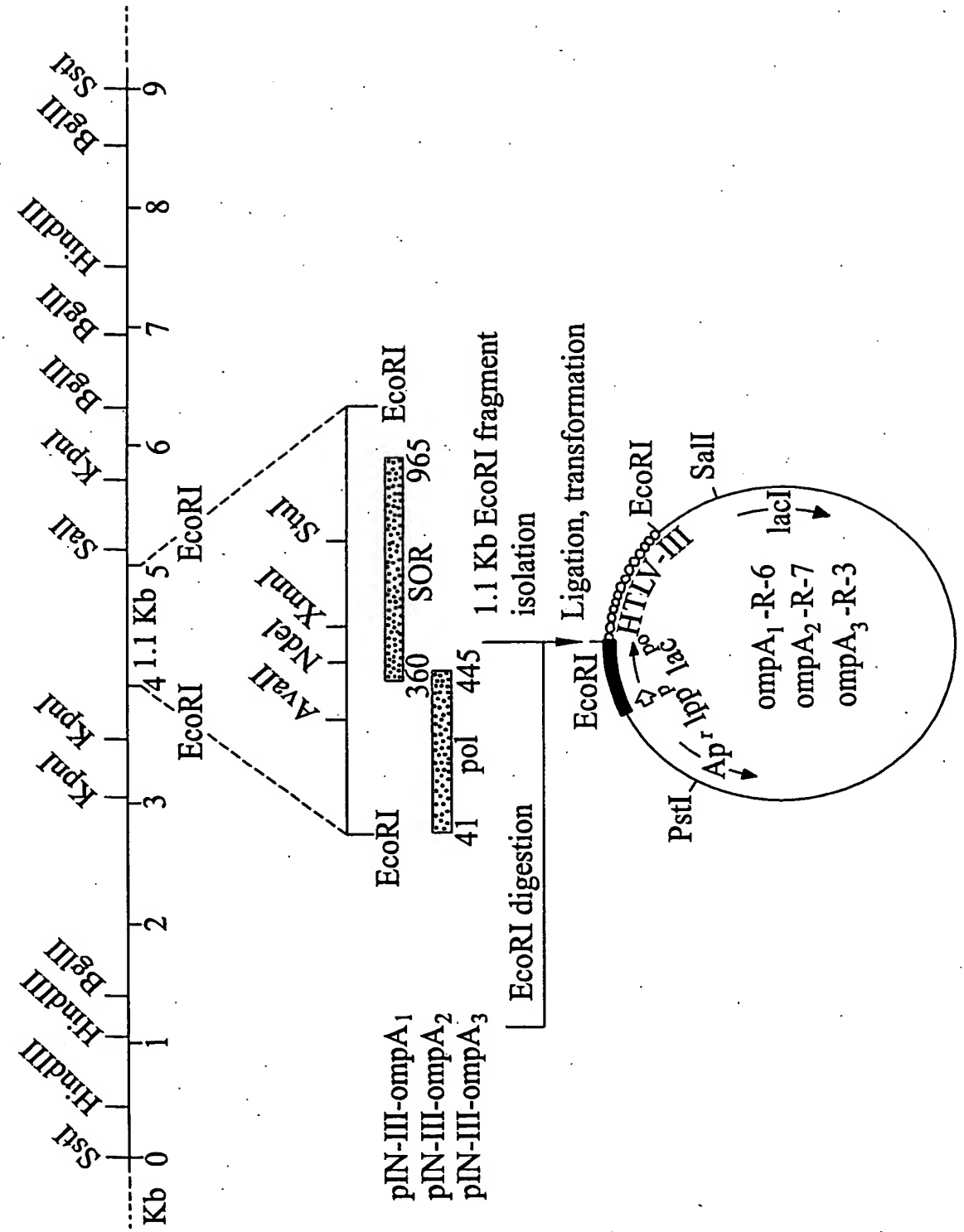

Kb 0 1 2 3 4 1.1 Kb 5 6 7 8 9
SstI
HindIII
HindIII
KpnI
KpnI
EcoRI
EcoRI
SalI
KpnI
BglII
BglII
HindIII
BglII
SstI
pIN-III-ompA1
pIN-III-ompA2
pIN-III-ompA3
EcoRI
41
pol
445
AvaII
NdeI
XmnI
StuI
360
SOR
965
EcoRI
EcoRI digestion
1.1 Kb EcoRI fragment
isolation
Ligation, transformation
EcoRI
HTLV-III
EcoRI
SalI
lacI
ompA1 -R-6
ompA2 -R-7
ompA3 -R-3
Ap r
lpp
lac
PstI

FIG. 5

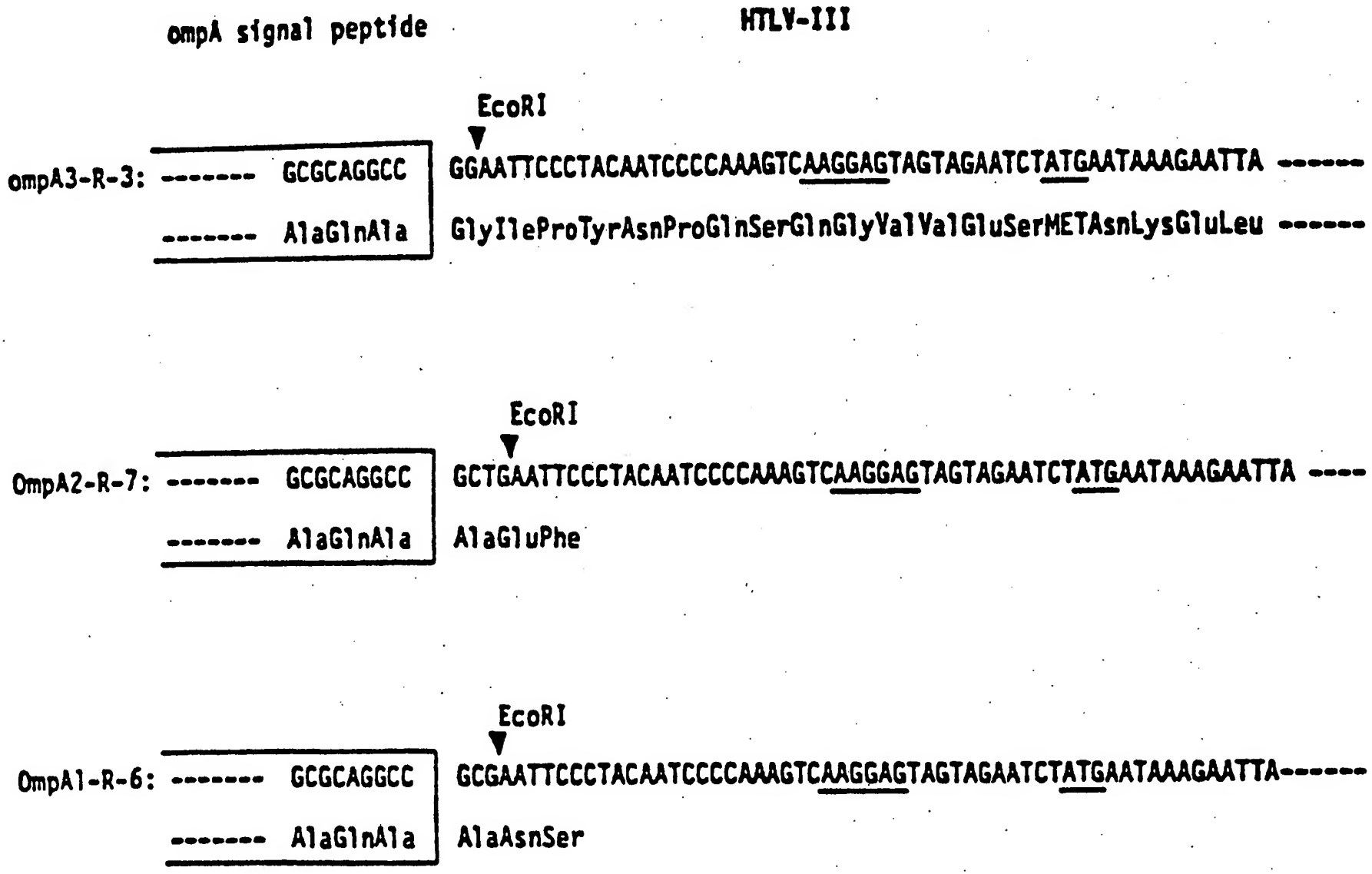
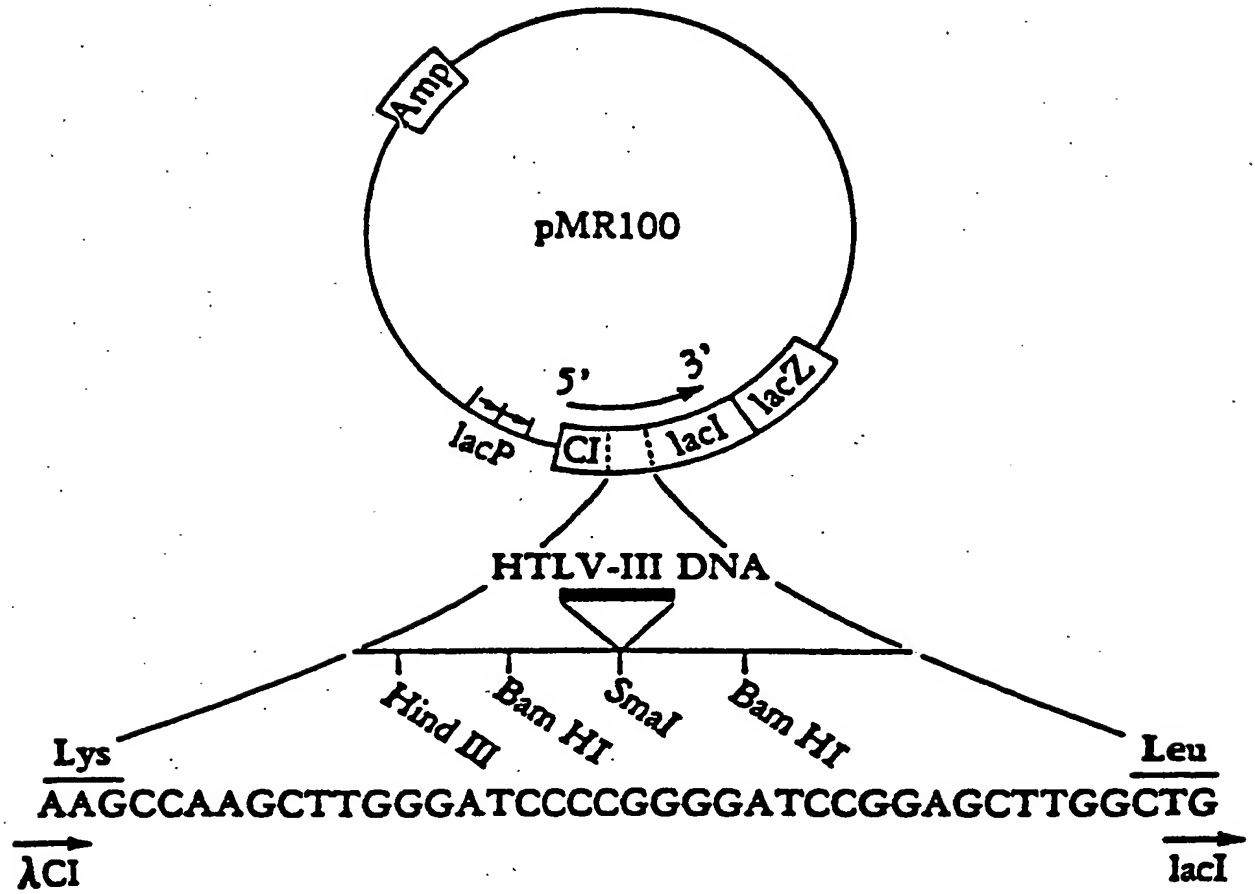

ompA signal peptide
HTLV-III
EcoRI
ompA3-R-3:
------- GCGCAGGCC
------- AlaGlnAla
GGAATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTA ------
GlyIleProTyrAsnProGlnSerGlnGlyValValGluSerMETAsnLysGluLeu ------
EcoRI
OmpA2-R-7:
------- GCGCAGGCC
------- AlaGlnAla
GCTGAATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTA ----
AlaGluPhe
EcoRI
OmpA1-R-6:
------- GCGCAGGCC
------- AlaGlnAla
GCGAATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCTATGAATAAAGAATTA------
AlaAsnSer

FIG. 6


Amp
pMR100
5'
3'
lacZ
lacP
CI
lacI
HTLV-III DNA
Hind III
Bam HI
SmaI
Bam HI
Lys
Leu
AAGCCAAGCTTGGGATCCCCGGGGATCCGGAGCTTGGCTG
λCI
lacI